

FIG. 1

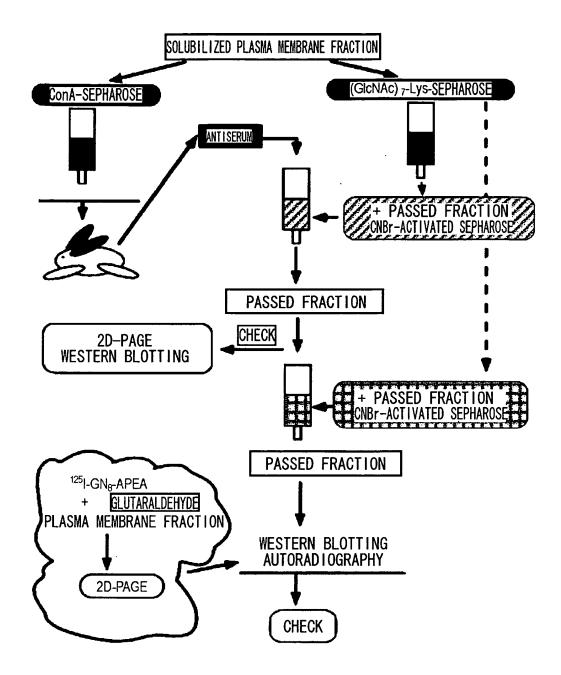


FIG. 2

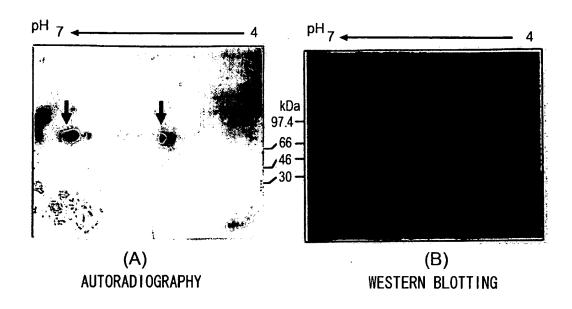


FIG. 3

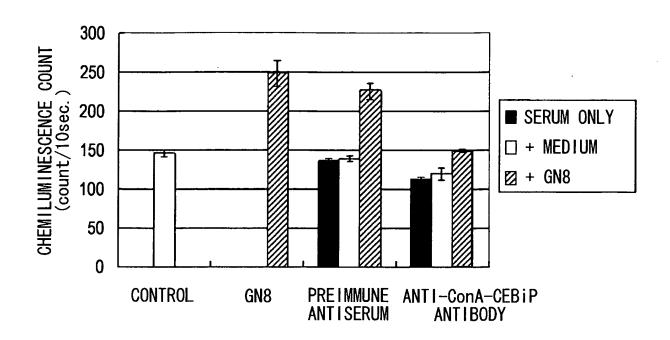
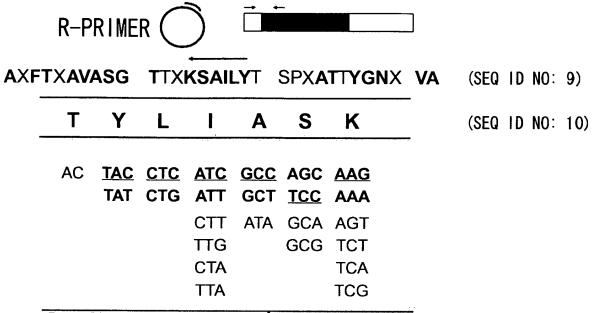


FIG. 4



*Temp: RICE cDNA LIBRARY (1 x 106 pfu)

FIG. 5

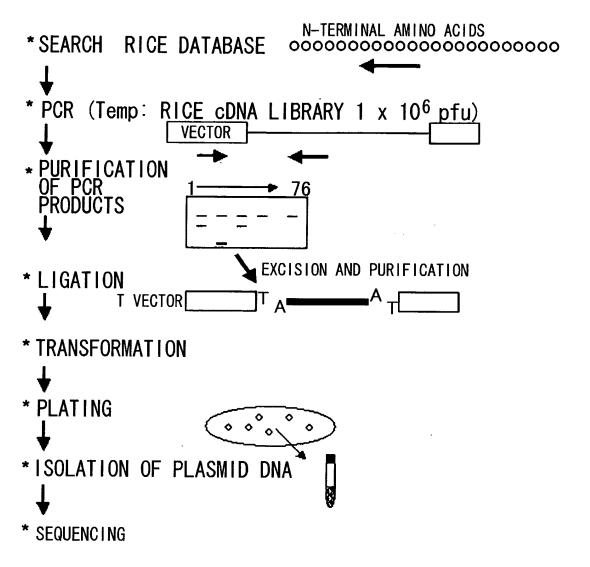


FIG. 6

TICCATCGGTAATTTTGAAATTTCAGTGATTTTTTGTTCTCCAAGTCTGACCAATCGAATCGAATCGAACCAAA	GTTCACCATTTTCTACTTTGATGCAATCGAACCAAA F T I F Y F D A I E P K	110	
GGATAGGGAAAGGCCCACGTGCAACCATTTAAGTGGCACAAGCACTAGCATGGGCATACTCCTGCTGCTGCAGTGAACAGGGGCAAACAAGAGCCT S P T L Q P F K S P Q A L A S R H T P P A P V S T R Q S N K H Q A S	CAGTGTCAACACGACAGCCT	220	
CTCATTCCCACCTCTCGAGGAGGTTTCCCCACCATGGCGTCGCTCGC	SECTECETECTCCTCGTCCTCGCCGCCCCC	330	
GCCTCCGCCGCCAACTTCACCTGCGGTGGCTTCAGGCACCTCCTGCAAGTCCGCCTCTTACACCTCCCCAACGCCACCTACGGCAACCTCGTCGCCGCTTT	CAACGCCACCACCTACGCCAACCTCGTCGCCCGCTT N A T T Y G N L V A R F	440 34	N-TERMINAL 32
CAACACCACCACCCCCCGACCTCCTCGGCCAACGCCTCCCCGACGCTTTCCTCCGCCCCTCGCCGCCAATTCCACCGTCAAAATCCCTTCCGCTGCC	CCGCCAATTCCACCGTCAAAATCCCCTTCCGCTGCC	550 71	RESIDUES
GCTGCAACGGCGACGTCGGCCCCCCCTCTCTACGTCGTGCAGCCGCAGGGCTCGACGCCTTCGCCGCAACGTGTTCAACGCCTTCGTCACCTACCT	ATCGCCCCAACGTGTCAACGCCTTGGTCACCTAC	107	
CAGGAGATGCCGCCGCGAACAACATCCCCGACCAACAAGATAAATGTCAGCCAGACGCTGTGGATTCCGCTGCACGCGCGCAGGAGGAGGCTCTAAGGT	GCCTGCAGCTGCGACAAGGAGGCTCTAACGT P C S C D K E E G S N V	770 144	LysM DOMAIN
GATGCACCTCGCCTACAGCGTCGCCAAAGGGGAGAACACGTCGGCGATCGCTGCCGGTGGGGGGGG	CCACGCTTCTCACAGAAATAAGATCGACGACCCA	88 2	DETERMINED INTERNAL AMINO ACID
CGAAATTGCAGATGGGACAGATTCTAGATGTCCCGCTCCTGTGTCATCATCAGCGATACCTCAGCTGATCAATCTGATGCTCCTCCCGGATGCCACTAT	GATCACAATCTGATGCTCCTCCCGGATGCCACCTAT D H N L M L L P D G T Y	990	SEQUENCE
GGATTCACCGCAGGAAACTGCATCGCTGCAGTTCAACTACCTAC	GAACAAGGGATGCCCGTCAGTGC N K G C P S V P L C N G	1100	
AACGCTGAAGCTTGGTGAGACGAACGGCACCGGTTGCGGATCAACAACGTGCGTG	GTTCATCGCTCATCAACCAGCCTTGCAACTA	1210 291	
ATCAGACAACACCTGCCAGAGGAGGAGGATCTGGGAGGTCGCAGGTCCATGTGGAGCATGTCTGTTATCTCCTTCCACATGGTGTTGATCATTATCTGTTTC	ATCTCCTTCCACATGGTGTTGATCATTATCTGTTTC	1320 32Z	PUTATIVE
CTTIGATGTIGGAGACTACTGGAACTCTAGATGGTACATITCAAAGAGTTCTCTACGATCTATGATTGTTGTATACGATATATGATTGTTGTCGTAACTTAGATTTTGAT	ACGATATATGATTGTTGTCGTAACTTAGATTTTGAT	1430	REGION REGION
GACTGGTTTATCCAGCTTTGAAATTTGAGTTTTGACTCTGTTCTTTAGAGGATGAGTGGCACTTGTACGGCTGCTTGAATAAAACGTCGATGTATTGTATTCGATCTGCA	TTGAATAAAACGTCGATGTATTGTATTCGATCTGCA	1540	
TCTGAAAAGGAATATTCATTAGATAGGATFATTCGAAATAAAAGATCCCACATGTTTTTGTTAAAAAAAA		1612	

FIG. 7

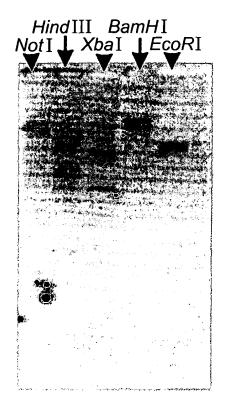


FIG. 8

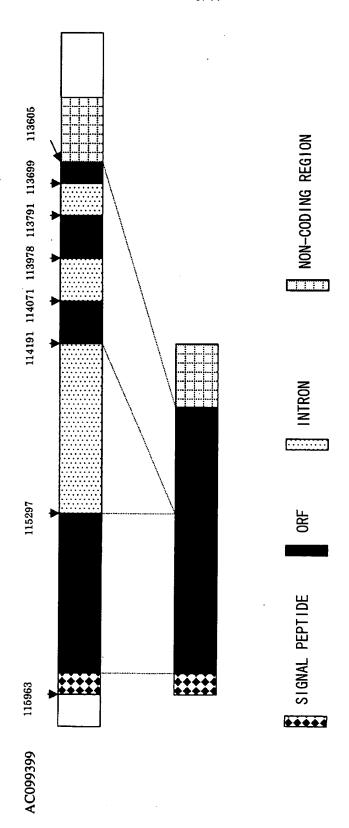


FIG. 9

GlcNAc7

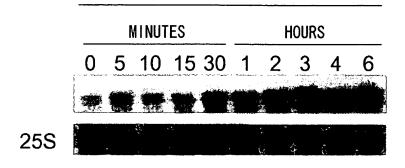
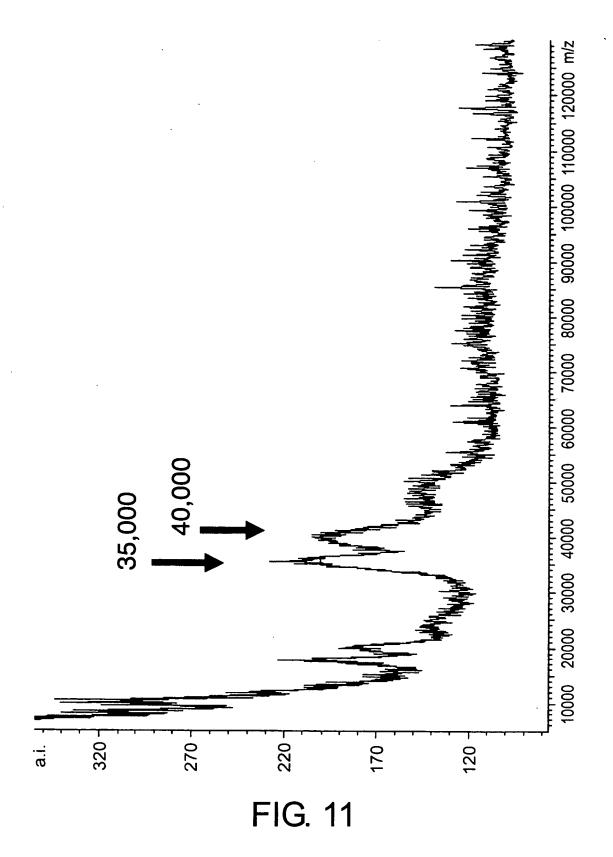


FIG. 10



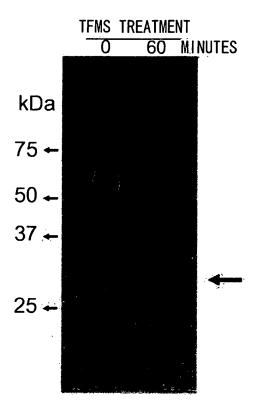


FIG. 12

5'-ACAGAACAAGGGATGCCCGTCAGTGCCACTGTGCAATGGAACGCTGAAGCT
TGGTGAGACGGCACCGGTTGCGGATCAACAACGTGCGCCTACAGTGGTTA
CTCCAACAGTTCATCGCTCATCATACAAACCAGCCTTGCAACTAATCAGACAAC
AGCCTGCCAGAGAGGAGGATCTGGGAGGTCGCAGTTCGCTAGGTCCATGTGGAG
CATGTCTGTTATCTCCTTCCACATGGTGTTGATCATTATCTGTTTCCTTTGATG
TTGGAGACTACTGCAACTCTAGATGGTACATTTCAAAGAGTTCTCTACGATCTA
TGATTGTTGTATACGATATATGATTGTTGTCGTAACTTAGATTTTGATGACTGG
TTTATCCAGC-3' (SEQ ID NO: 13)

FIG. 13

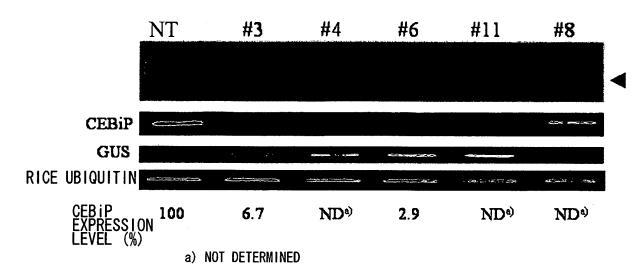
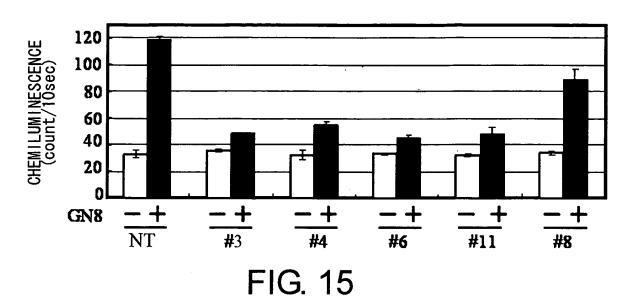


FIG. 14



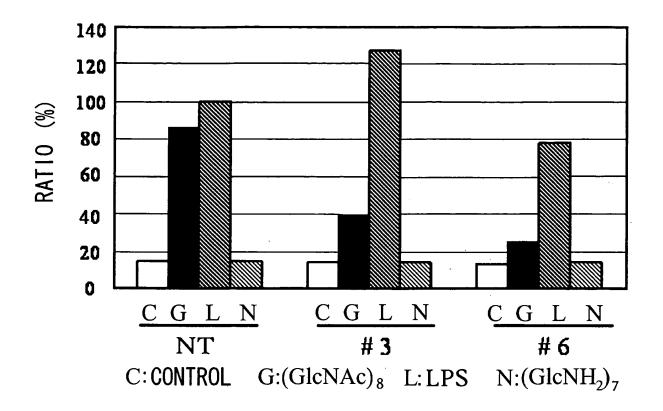
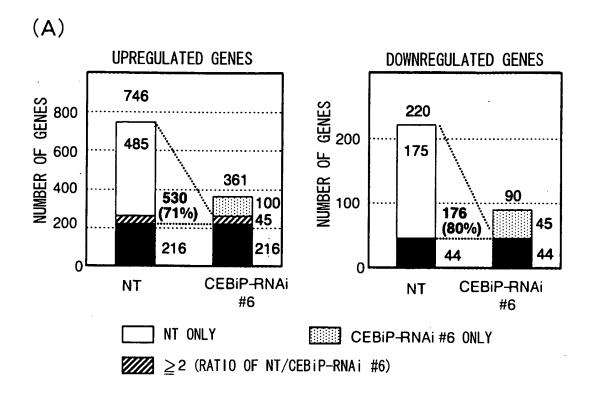


FIG. 16



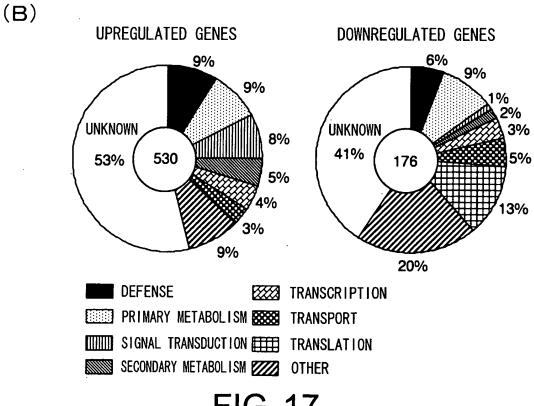


FIG. 17